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5-2-02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/687,837

DATE: 04/23/2002 P.5

TIME: 09:34:13

Input Set : A:\20054210.app

Output Set: N:\CRF3\04232002\I687837.raw

3 <110> APPLICANT: Lu, Peter S.
4 Carman, Jonathan D.
5 Candia III, Albert F.
6 Arbbor Vita Corporation
8 <120> TITLE OF INVENTION: CLASP-2 TRANSMEMBRANE PROTEINS
10 <130> FILE REFERENCE: 020054-000210US
12 <140> CURRENT APPLICATION NUMBER: US 09/687,837
13 <141> CURRENT FILING DATE: 2000-10-13
15 <150> PRIOR APPLICATION NUMBER: US 60/129,171
16 <151> PRIOR FILING DATE: 1999-04-14
18 <150> PRIOR APPLICATION NUMBER: US 60/134,114
19 <151> PRIOR FILING DATE: 1999-05-14
21 <150> PRIOR APPLICATION NUMBER: US 60/134,118
22 <151> PRIOR FILING DATE: 1999-05-14
24 <150> PRIOR APPLICATION NUMBER: US 60/160,860
25 <151> PRIOR FILING DATE: 1999-10-21
27 <150> PRIOR APPLICATION NUMBER: US 60/162,498
28 <151> PRIOR FILING DATE: 1999-10-29
30 <150> PRIOR APPLICATION NUMBER: US 60/170,453
31 <151> PRIOR FILING DATE: 1999-12-13
33 <150> PRIOR APPLICATION NUMBER: US 60/176,195
34 <151> PRIOR FILING DATE: 2000-01-14
36 <150> PRIOR APPLICATION NUMBER: US 60/182,296
37 <151> PRIOR FILING DATE: 2000-02-14
39 <150> PRIOR APPLICATION NUMBER: US 09/547,276
40 <151> PRIOR FILING DATE: 2000-04-11
42 <150> PRIOR APPLICATION NUMBER: US 60/134,117
43 <151> PRIOR FILING DATE: 1999-05-14
45 <160> NUMBER OF SEQ ID NOS: 152
47 <170> SOFTWARE: PatentIn Ver. 2.1
49 <210> SEQ ID NO: 1
50 <211> LENGTH: 4807
51 <212> TYPE: DNA
52 <213> ORGANISM: Homo sapiens
54 <220> FEATURE:
55 <221> NAME/KEY: CDS
56 <222> LOCATION: (2)..(4060)
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Human cadherin-like asymmetry protein 2A
60 (CLASP-2A)
62 <400> SEQUENCE: 1
63 a gtt tta cac cat cac caa aac cca gaa ttt tat gat gag att aaa ata 49
64 Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile

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68	Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe				
69	20 25 30				
71	ttc cat gtc agc tgt gac aac tca agt aaa gga agc acg aag aag agg	145			
72	Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg				
73	35 40 45				
75	gat gtc gtt gaa acc caa gtt ggc tac tcc tgg ctt ccc ctc ctg aaa	193			
76	Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys				
77	50 55 60				
79	gac gga agg gtg gtg aca agc gag cag cac atc ccg gtc tcg gcg aac	241			
80	Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn				
81	65 70 75 80				
83	ctt cct tcg ggc tat ctt ggc tac caa gag ctt ggg atg ggc agg cat	289			
84	Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His				
85	85 90 95				
87	tat ggt ccg gaa att aaa tgg gta gat gga ggc aag cca ctg ctg aaa	337			
88	Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys				
89	100 105 110				
91	att tcc act cat ctg gtt tct aca gtg tat act cag gat cag cat tta	385			
92	Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu				
93	115 120 125				
95	cat aat ttt ttc cag tac tgt cag aaa acc gaa tct gga gcc caa gcc	433			
96	His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala				
97	130 135 140				
99	tta gga aac gaa ctt gta aag tac ctt aag agt ctg cat gcg atg gaa	481			
100	Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu				
101	145 150 155 160				
103	ggc cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc	529			
104	Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe				
105	165 170 175				
107	cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act	577			
108	Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr				
109	180 185 190				
111	cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag	625			
112	Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu				
113	195 200 205				
115	agc cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat	673			
116	Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr				
117	210 215 220				
119	gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg	721			
120	Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met				
121	225 230 235 240				
123	acc acg att ctc aag cct tct gcc gat ttc ctc acc agc aac aaa cta	769			
124	Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu				
125	245 250 255				
127	ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct	817			
128	Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala				
129	260 265 270				

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133			275					280					285				
135	ttt	cct	gca	tcc	tat	cat	cat	gca	gcg	gaa	acc	ggt	gta	aat	atg	ctg	913
136	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	
137		290					295					300					
139	atg	cca	cac	atc	act	cag	aag	ttt	gga	gat	aat	cca	gag	gca	tct	aag	961
140	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	
141	305					310				315					320		
143	aac	gcg	aat	cat	agc	ctt	gct	gtc	ttc	atc	aag	aga	tgt	ttc	acc	ttc	1009
144	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	
145				325					330					335			
147	atg	gac	agg	ggc	ttt	gtc	ttc	aag	cag	atc	aac	aac	tac	att	agc	tgt	1057
148	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	
149			340					345					350				
151	ttt	gct	cct	gga	gac	cca	aag	acc	ctc	ttt	gaa	tac	aag	ttt	gaa	ttt	1105
152	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	
153			355					360					365				
155	ctc	cgt	gta	gtg	tgc	aac	cat	gaa	cat	tat	att	ccg	ttg	aac	tta	cca	1153
156	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	
157		370				375						380					
159	atg	cca	ttt	gga	aaa	ggc	agg	att	caa	aga	tac	caa	gac	ctc	cag	ctt	1201
160	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	
161	385					390				395					400		
163	gac	tac	tca	tta	aca	gat	gag	ttc	tgc	aga	aac	cac	ttc	ttg	gtg	gga	1249
164	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	
165				405				410					415				
167	ctg	tta	ctg	agg	gag	gtg	ggg	aca	gcc	ctc	cag	gag	ttc	cgg	gag	gtc	1297
168	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	
169				420				425					430				
171	cgt	ctg	atc	gcc	atc	agt	gtg	ctc	aag	aac	ctg	ctg	ata	aag	cat	tct	1345
172	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	
173			435					440					445				
175	ttt	gat	gac	aga	tat	gct	tca	agg	agc	cat	cag	gca	agg	ata	gcc	acc	1393
176	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	
177		450				455					460						
179	ctc	tac	ctg	cct	ctg	ttt	ggt	ctg	ctg	att	gaa	aac	gtc	cag	cgg	atc	1441
180	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	
181	465					470				475						480	
183	aat	gtg	agg	gat	gtg	tca	ccc	ttc	cct	gtg	aac	gcg	ggc	atg	acc	gtg	1489
184	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	
185				485				490					495				
187	aag	gat	gaa	tcc	ctg	gct	cta	cca	gct	gtg	aat	ccg	ctg	gtg	acg	ccg	1537
188	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	
189			500					505					510				
191	cag	aag	gga	agc	acc	ctg	gac	aac	agc	ctg	cac	aag	gac	ctg	ctg	ggc	1585
192	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	
193			515					520					525				
195	gcc	atc	tcc	ggc	att	gct	tct	cca	tat	aca	acc	tca	act	cca	aac	atc	1633

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196	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	
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199	aac	agt	gtg	aga	aat	gct	gat	tcg	aga	gga	tct	ctc	ata	agc	aca	gat	1681
200	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	
201	545					550					555					560	
203	tcg	ggt	aac	agc	ctt	cca	gaa	agg	aat	agt	gag	aag	agc	aat	tcc	ctg	1729
204	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu	
205					565						570					575	
207	gat	aag	cac	caa	caa	agt	agc	aca	ttg	gga	aat	tcc	gtg	ggt	cgc	tgt	1777
208	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys	
209				580					585					590			
211	gat	aaa	ctt	gac	cag	tct	gag	att	aag	agc	cta	ctg	atg	tgt	ttc	ctc	1825
212	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	
213			595					600					605				
215	tac	atc	tta	aag	agc	atg	tct	gat	gat	gct	ttg	ttt	aca	tat	tgg	aac	1873
216	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	
217		610					615					620					
219	aag	gct	tca	aca	tct	gaa	ctt	atg	gat	ttt	ttt	aca	ata	tct	gaa	gtc	1921
220	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val	
221	625					630					635					640	
223	tgc	ctg	cac	cag	ttc	cag	tac	atg	ggg	aag	cga	tac	ata	gcc	agg	aac	1969
224	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn	
225				645						650					655		
227	cag	gag	ggg	ttg	gga	ccc	ata	gtt	cat	gat	cga	aag	tct	cag	aca	ttg	2017
228	Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	Thr	Leu	
229				660					665					670			
231	cct	gtt	tcc	cgt	aac	aga	aca	gga	atg	atg	cat	gcc	aga	ttg	cag	cag	2065
232	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	
233			675					680					685				
235	ctg	ggc	agc	ctg	gat	aac	tct	ctc	act	ttt	aac	cac	agc	tat	ggc	cac	2113
236	Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	
237		690					695				700						
239	tcg	gac	gca	gat	gtt	ctg	cac	cag	tca	tta	ctt	gaa	gcc	aac	att	gct	2161
240	Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	
241	705					710					715					720	
243	act	gag	gtt	tgc	ctg	aca	gct	ctg	gac	acg	ctt	tct	cta	ttt	aca	ttg	2209
244	Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	
245				725						730					735		
247	gcg	ttt	aag	aac	cag	ctc	ctg	gcc	gac	cat	gga	cat	aat	cct	ctc	atg	2257
248	Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	
249				740					745					750			
251	aaa	aaa	gtt	ttt	gat	gtc	tac	ctg	tgt	ttt	ctt	caa	aaa	cat	cag	tct	2305
252	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	
253			755					760						765			
255	gaa	acg	gct	tta	aaa	aat	gtc	ttc	act	gcc	tta	agg	tcc	tta	att	tat	2353
256	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	
257		770					775					780					
259	aag	ttt	ccc	tca	aca	ttc	tat	gaa	ggg	aga	gcg	gac	atg	tgt	gcg	gct	2401
260	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	

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263	ctg	tgt	tac	gag	att	ctc	aag	tgc	tgt	aac	tcc	aag	ctg	agc	tcc	atc	2449
264	Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	
265						805				810					815		
267	agg	acg	gag	gcc	tcc	cag	ctg	ctc	tac	ttc	ctg	atg	agg	aac	aac	ttt	2497
268	Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	
269						820				825					830		
271	gat	tac	act	gga	aag	aag	tcc	ttt	gtc	cgg	aca	cat	ttg	caa	gtc	atc	2545
272	Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	
273						835				840					845		
275	ata	tct	gtc	agc	cag	ctg	ata	gca	gac	gtt	gtt	ggc	att	ggg	gaa	acc	2593
276	Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr	
277						850				855					860		
279	aga	ttc	cag	cag	tcc	ctg	tcc	atc	atc	aac	aac	tgt	gcc	aac	agt	gac	2641
280	Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp	
281	865					870				875					880		
283	cgg	ctt	att	aag	cac	acc	agc	ttc	tcc	tct	gat	gtg	aag	gac	tta	acc	2689
284	Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr	
285						885				890					895		
287	aaa	agg	ata	cgc	acg	gtg	cta	atg	gcc	acc	gcc	cag	atg	aag	gag	cat	2737
288	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	
289						900				905					910		
291	gag	aac	gac	cca	gag	atg	ctg	gtg	gac	ctc	cag	tac	agc	ctg	gcc	aaa	2785
292	Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	
293						915				920					925		
295	tcc	tat	gcc	agc	acg	ccc	gag	ctc	agg	aag	acg	tgg	ctc	gac	agc	atg	2833
296	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	
297						930				935					940		
299	gcc	agg	atc	cat	gtc	aaa	aat	ggc	gat	ctc	tca	gag	gca	gca	atg	tgc	2881
300	Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	
301	945					950				955					960		
303	tat	gtc	cac	gta	aca	gcc	cta	gtg	gca	gaa	tat	ctc	aca	cgg	aaa	ggc	2929
304	Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Gly	
305						965				970					975		
307	gtg	ttt	aga	caa	gga	tgc	acc	gcc	ttc	agg	gtc	att	acc	cca	aac	atc	2977
308	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn	Ile	
309						980				985					990		
311	gac	gag	gag	gcc	tcc	atg	atg	gaa	gac	gtg	ggg	atg	cag	gat	gtc	cat	3025
312	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	Val	His	
313						995				1000					1005		
315	ttc	aac	gag	gat	gtg	ctg	atg	gag	ctc	ctt	gag	cag	tgc	gca	gat	gga	3073
316	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp	Gly	
317						1010				1015					1020		
319	ctc	tgg	aaa	gcc	gag	cgc	tac	gag	ctc	atc	gcc	gac	atc	tac	aaa	ctt	3121
320	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys	Leu	
321	1025					1030				1035					1040		
323	atc	atc	ccc	att	tat	gag	aag	cgg	agg	gat	ttc	ttt	gaa	gat	gaa	gat	3169
324	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	Glu	Asp	
325						1045				1050					1055		

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\20054210.app

Output Set: N:\CRF3\04232002\I687837.raw

L:5199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:5229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:5237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:5238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:5239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:5240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:5259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:5295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:5305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:5330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:5364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:5366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:5392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:5421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:5423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:5424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/687,837

DATE: 04/23/2002

TIME: 09:34:14

Input Set : A:\20054210.app

Output Set: N:\CRF3\04232002\I687837.raw

L:5425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75

L:5451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76